



results of BLAST

BLASTP 2.2.14 [May-07-2006]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1150326844-7029-23201072992.BLASTQ4

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples
3,695,564 sequences; 1,269,795,892 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

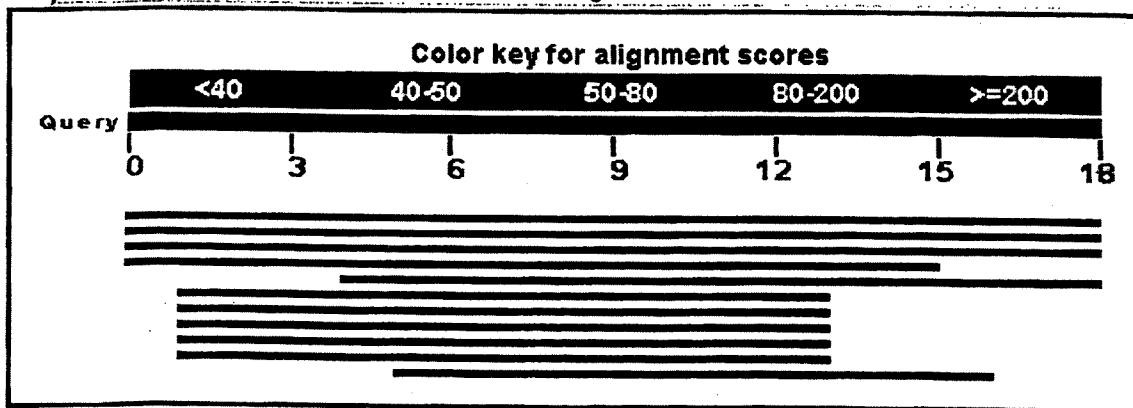
[Taxonomy reports](#)

Query=

Length=18

Distribution of 11 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments



[Free view NEW](#)

Sequences producing significant alignments:

		Score (Bits)	E Value	
gi 54696716 gb AAV38730.1	tumor necrosis factor receptor sup...	56.2	1e-07	6
gi 339758 gb AAA36755.1	tumor necrosis factor receptor	56.2	1e-07	6
gi 37359212 gb AAN72434.1	soluble tumor necrosis factor rece...	56.2	1e-07	6
gi 825701 emb CAA56324.1	p75 TNF receptor [Homo sapiens]	46.4	1e-04	5
gi 6683130 dbj BAA89052.1	tumor necrosis factor receptor 2 [Hom	43.9	8e-04	5
gi 15030259 gb AAH11399.1	SYK protein [Homo sapiens] >gi 559...	28.6	30	5
gi 515871 emb CAA51970.1	protein tyrosin kinase [Homo sapiens]	28.6	30	5

EXHIBIT D

<u>gi 12804475 gb AAH01645.1 </u>	Spleen tyrosine kinase [Homo sapi...	<u>28.6</u>	30	
<u>gi 448916 prf 1918215A </u>	protein Tyr kinase	<u>28.6</u>	30	
<u>gi 1092813 prf 2101280A </u>	p72syk protein	<u>28.6</u>	30	
<u>gi 89061682 ref XP_944591.1 </u>	PREDICTED: similar to dynein, ax...	<u>26.1</u>	174	

Alignments

Get selected sequences Select all Deselect all Tree View

> gi|54696716|gb|AAV38730.1| tumor necrosis factor receptor superfamily, member
gi|31419790|gb|AAH52977.1| Tumor necrosis factor receptor 2, precursor [Homo sap
gi|32891819|gb|AAP88939.1| tumor necrosis factor receptor superfamily, member 1B
gi|55663791|emb|CAH73721.1| tumor necrosis factor receptor superfamily, member 1
gi|56202703|emb|CAI19225.1| tumor necrosis factor receptor superfamily, member 1
gi|4507577|ref|NP_001057.1| tumor necrosis factor receptor 2 precursor [Homo sap
gi|29725900|gb|AAO89076.1| tumor necrosis factor receptor superfamily, member 1B
gi|61356471|gb|AAX41249.1| tumor necrosis factor receptor superfamily member 1B [s
construct]
gi|21264534|sp|P20333|TNR1B_HUMAN Tumor necrosis factor receptor superfamily mem
(Tumor necrosis factor receptor 2) (TNF-R2) (Tumor necrosis
factor receptor type II) (p75) (p80 TNF-alpha receptor) (CD120b
antigen) (Etanercept) [Contains: Tumor necrosis factor
receptor superfamily member 1b, membrane form; Tumor necrosis
factor-binding protein 2 (TBPII) (TBP-2)]
gi|1469541|gb|AAC50622.1| tumor necrosis factor receptor
gi|189186|gb|AAA59929.1| tumor necrosis factor receptor
Length=461

Score = 56.2 bits (125), Expect = 1e-07
Identities = 17/18 (94%), Positives = 17/18 (94%), Gaps = 0/18 (0%)

Query 1 LPAQVAFBPYAPEPGSTC 18
LPAQVAF PYAPEPGSTC
Sbjct 23 LPAQVAFTPYAPEPGSTC 40

> gi|339758|gb|AAA36755.1| tumor necrosis factor receptor
Length=461

Score = 56.2 bits (125), Expect = 1e-07
Identities = 17/18 (94%), Positives = 17/18 (94%), Gaps = 0/18 (0%)

Query 1 LPAQVAFBPYAPEPGSTC 18
LPAQVAF PYAPEPGSTC
Sbjct 23 LPAQVAFTPYAPEPGSTC 40

> gi|37359212|gb|AAN72434.1| soluble tumor necrosis factor receptor superfamily
[Homo sapiens]
Length=268

Score = 56.2 bits (125), Expect = 1e-07
Identities = 17/18 (94%), Positives = 17/18 (94%), Gaps = 0/18 (0%)

Query 1 LPAQVAFBPYAPEPGSTC 18
LPAQVAF PYAPEPGSTC

Sbjct 23 LPAQVAFTPYAPEPGSTC 40

> gi|825701|emb|CAA56324.1| p75 TNF receptor [Homo sapiens]
Length=37

Score = 46.4 bits (102), Expect = 1e-04
Identities = 14/15 (93%), Positives = 14/15 (93%), Gaps = 0/15 (0%)

Query 1 LPAQVAFBPYAPEPG 15
LPAQVAF PYAPEPG
Sbjct 23 LPAQVAFBPYAPEPG 37

> gi|6683130|dbj|BAA89052.1| tumor necrosis factor receptor 2 [Homo sapiens]
Length=33

Score = 43.9 bits (96), Expect = 8e-04
Identities = 13/14 (92%), Positives = 13/14 (92%), Gaps = 0/14 (0%)

Query 5 VAFBPYAPEPGSTC 18
VAF PYAPEPGSTC
Sbjct 1 VAFTPYAPEPGSTC 14

> gi|15030259|gb|AAH11399.1| SYK protein [Homo sapiens]
gi|55958427|emb|CAI16875.1| spleen tyrosine kinase [Homo sapiens]
gi|496900|emb|CAA82737.1| protein-tyrosine kinase [Homo sapiens]
Length=612

Score = 28.6 bits (60), Expect = 30
Identities = 9/19 (47%), Positives = 11/19 (57%), Gaps = 7/19 (36%)

Query 2 PAQ-----VAFBPYAPE 13
PAQ V+F+PY PE
Sbjct 285 PAQGNRQESTVSFNPYEPE 303

> gi|515871|emb|CAA51970.1| protein tyrosin kinase [Homo sapiens]
Length=630

Score = 28.6 bits (60), Expect = 30
Identities = 9/19 (47%), Positives = 11/19 (57%), Gaps = 7/19 (36%)

Query 2 PAQ-----VAFBPYAPE 13
PAQ V+F+PY PE
Sbjct 303 PAQGNRQESTVSFNPYEPE 321

> gi|12804475|gb|AAH01645.1| Spleen tyrosine kinase [Homo sapiens]
gi|55958428|emb|CAI16876.1| spleen tyrosine kinase [Homo sapiens]
gi|1174527|sp|P43405|KSYK_HUMAN| Tyrosine-protein kinase SYK (Spleen tyrosine kin
gi|12804209|gb|AAH02962.1| Spleen tyrosine kinase [Homo sapiens]
gi|21361553|ref|NP_003168.2| spleen tyrosine kinase [Homo sapiens]
gi|479013|gb|AAA36526.1| protein tyrosine kinase
Length=635

Score = 28.6 bits (60), Expect = 30
Identities = 9/19 (47%), Positives = 11/19 (57%), Gaps = 7/19 (36%)

Query 2 PAQ-----VAFBPYAPE 13
 PAQ V+F+PY PE
 Sbjct 308 PAQGNRQESTVSFNPYEP 326

> gi|448916|prf||1918215A protein Tyr kinase
 Length=630

Score = 28.6 bits (60), Expect = 30
 Identities = 9/19 (47%), Positives = 11/19 (57%), Gaps = 7/19 (36%)

Query 2 PAQ-----VAFBPYAPE 13
 PAQ V+F+PY PE
 Sbjct 303 PAQGNRQESTVSFNPYEP 321

> gi|1092813|prf||2101280A p72syk protein
 Length=365

Score = 28.6 bits (60), Expect = 30
 Identities = 9/19 (47%), Positives = 11/19 (57%), Gaps = 7/19 (36%)

Query 2 PAQ-----VAFBPYAPE 13
 PAQ V+F+PY PE
 Sbjct 303 PAQGNRQESTVSFNPYEP 321

> gi|89061682|ref|XP_944591.1| PREDICTED: similar to dynein, axonemal, heavy pol
 sapiens]
 Length=4107

Score = 26.1 bits (54), Expect = 174
 Identities = 9/15 (60%), Positives = 9/15 (60%), Gaps = 4/15 (26%)

Query 6 AFBP---YAPEPGS 16
 AF P Y PEPGS
 Sbjct 3866 AFSPSGLYTPEPGS 3880

Get selected sequences Select all Deselect all Tree View

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples

Posted date: Jun 10, 2006 4:09 AM

Number of letters in database: 1,269,795,892

Number of sequences in database: 3,695,564

Lambda K H
 0.346 0.288 1.79

Gapped

Lambda K H
 0.294 0.110 0.610

Matrix: PAM30

Gap Penalties: Existence: 9, Extension: 1

Number of Sequences: 3695564

Number of Hits to DB: 15358398

Number of extensions: 349668

Number of successful extensions: 1740

Number of sequences better than 20000: 1713

Number of HSP's better than 20000 without gapping: 0
Number of HSP's gapped: 1740
Number of HSP's successfully gapped: 1740
Length of query: 18
Length of database: 1269795892
Length adjustment: 8
Effective length of query: 10
Effective length of database: 1240231380
Effective search space: 12402313800
Effective search space used: 12402313800
T: 11
A: 40
X1: 15 (7.5 bits)
X2: 35 (14.8 bits)
X3: 58 (24.6 bits)
S1: 38 (19.3 bits)
S2: 38 (19.3 bits)